

Subsequent BSI developed in 6 (20%) of 30 episodes in which empiric antibiotic treatment were inappropriate while but in 3 (4%) of 82 episodes in which empiric antibiotic treatment were appropriate ($P = .01$).

Conclusion: In patients with isolated positive HC-drawn blood cultures, the overall incidence of subsequent BSI was 8.0%. Isolation of *Candida* species and inappropriate empiric treatment were associated with development of subsequent BSI.

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Prevalence and factors associated with hospital acquired infections in Kayunga district hospital, central Uganda

R. Ankunda^{1,*}, D. Musisi², R. Tweheyo¹, O. Namusisi³

¹ Makerere University School of Public Health, Kampala, Kampala, Uganda

² Department of Health, Kayunga district, Kayunga, Uganda

³ African Field Epidemiology Network, kampala, Uganda

Background: Globally about 2 million people annually suffer Hospital Acquired Infections (HAIs), mainly patients hospitalized for other conditions leading to prolonged stay, increased morbidity and mortality. The magnitude of HAIs in Kayunga district hospital (KDH) was unknown in 2009; however, it is acknowledged that the lack of basic equipment and infrastructure compromises infection control practice making transmission of HAIs favorable. This study set out to estimate the prevalence and assess factors associated with HAIs in Kayunga district hospital (KDH) to enable the hospital management design interventions to address HAIs.

Methods: We conducted a cross sectional survey in the first week of July 2009 in Kayunga district hospital; - with 100 bed capacity. One hundred in-patients who had spent at least 72 hours were recruited consecutively into the study. Face-to-face interviews with study participants were conducted using a structured questionnaire and an observational check list filled on each ward. Ministry of Health, Epidemiological and Surveillance case definitions were used to identify new infections categorized as HAIs based on the disease-specific incubation period. Data was analyzed using SPSS version 12.0; the primary outcome was having a HAI.

Results: The prevalence of HAIs was 34.0% (34/100). Majority cases of HAIs had multiple infections (26.5%), followed by single infections; Respiratory tract infections (23.5%), Diarrhoea (17.6%), Urinary tract infections (14.7%) and others. Infection control practice on the wards was compromised by lack of hand washing facilities, lack of an isolation ward and lack of supplies for disinfection. HAIs in KDH were associated with having a surgical procedure at the current admission (OR 2.68, 95% CI: 1.10–6.53).

Conclusion: The prevalence of HAIs in KDH is high necessitating enforcement and monitoring of infection control practices in the hospital. Creation of an isolation unit for highly communicable diseases in the KDH should be offered priority. The District Health Team should lobby to ensure that flowing piped water is available in KDH. Active surveillance of HAIs among Post operative patients should be instituted. There is need for a study to investigate the relationship between having surgery and developing

a HAI.

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Vancomycin-resistant enterococci cross-transmission among patients admitted to public and private hospitals in central Brazil

M.A. Souza¹, A.O. Guilarde¹, M. Turchi¹, M.C.D.P.B. André¹, J.L. Cardoso¹, S.A.S. Paiva², C.A. Kobayashi³, C.X. Carvalho¹, G.S. Leal¹, A. Kipnis¹, J.D.G. Vieira¹, L.J.A. Batista¹, A.L. Andrade^{1,*}

¹ Federal University of Goiás, Goiania, Brazil

² INGOH, Goiania, Brazil

³ Goiás Health State Secretariat, Goiania, Brazil

Background: Enterococci harbouring a vancomycin resistance gene have emerged as an important nosocomial pathogen associated with high mortality. In Brazil, vancomycin-resistant enterococci (VRE) infection was first reported in the late 90 s, in the South region. In August 2007 the first case of VRE was identified in the city of Goiania (~1 million inhabitants), Central Brazil. We herein present the molecular characteristics of VRE isolated two years apart from its first isolation in our municipality.

Methods: Screening for VRE was performed in the two major public hospitals and one private hospital. Microbiological samples (rectal swabs, blood, urine, surgical specimens) were collected from adult patients admitted to clinical and surgical wards and Intensive Care Units (ICU). Suspected VRE colonies were submitted to identification using conventional biochemical tests and antimicrobial susceptibility (CLSI, 2008). Detection of vancomycin resistance genes was performed by PCR. The genetic relatedness of bacterial strains was evaluated by PFGE and the results were analyzed using Tenover criteria and BioNumerics (v. 5.0.).

Results: A total of 58 VRE (41 *E. faecium* and 17 *E. faecalis*) were isolated from 58 patients. Patients' age ranged from 13 to 84 years (median of 54 years). 76.5% of *E. faecalis* represented colonization (rectal swab) in contrast, almost half of *E. faecium* were associated with infection (blood, urine or surgical wound secretion). All VRE strains carried the *vanA* gene. 27 out of 41 (65.8%) strains of *E. faecium* belonged to the same cluster (genetic similarity $\geq 80\%$) and to 5 lineages highly related. Strains from private hospital were identical and not correlated to the ones from public hospitals. *E. faecalis* strains were classified in 5 clusters. 10.3% of the samples were susceptible to ampicillin and 86.2% to linezolid.

Conclusion: The study discloses the presence of VRE genetically related strains in distinct hospitals, suggesting cross-transmission intra and inter-hospitals. Genotyping surveillance is an important tool for understanding transmission patterns and for guiding infection control interventions.

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